

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/004,502

DATE: 12/12/2001
TIME: 14:28:17

Input Set : A:\BB1470 US NA Seq listing.txt
Output Set: N:\CRF3\12112001\I004502.raw

ENTERED

2 <110> APPLICANT: Harvell, Leslie T.
3 Ragghianti, James J
W--> 5 <110> APPLICANT:
7 <130> FILE REFERENCE: BB1470 US NA
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/004,502
C--> 10 <141> CURRENT FILING DATE: 2001-10-30
12 <150> PRIOR APPLICATION NUMBER: 60/244,272
13 <151> PRIOR FILING DATE: 2000-10-30
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: Microsoft Office 97
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1493
21 <212> TYPE: DNA
22 <213> ORGANISM: Zea mays
24 <400> SEQUENCE: 1
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26 tctcttctcg taaccgctgc cacctcgag cagcaagcaa gcgcgaccaa atggcgccctc 120
27 taggagacgg cggagctgct gccgcggcgg cgtccaacaa cctggtggtg tcgttcggcg 180
28 agatgctgat cgacttcgtc cccgacgtgg cggggtgtgc gctggccgag tcggggcggt 240
29 tcgtcaaggc ccccgcgggc gcgcgcgcca acgtcgccctg cgccatcgcc aagctcgggc 300
30 gatcctccgc cttcgctcggc aagttcggcg acgacgagtt cgggcacatg ttggtgaaca 360
31 tcctgaagca gaacaacgtg aactcggagg ggtgcctgtt cgacaagcac gcgcggacgg 420
32 cgctggcctt cgtgacgtc aagcacgacg gggagcgcga gttcatgttc tacaggaacc 480
33 cgagcgcgga catgctgctg acggaggcgg agctggacct gggcctggtg cggcgcgcca 540
34 aggtgttcca ctacggctcc atctcgctca tctccgagcc gtgccgctcg gcgcacatgg 600
35 ccgccatgcg cgcagccaag gccgcggggc tgcctctgtc ctacgacccc aacgtgcgcc 660
36 tcccgtctctg gccgtgcgcc gacgccgcac gcgagggcat cctcagcatc tggaaggagg 720
37 ccgacttcat caaggtcagc gacgacgagg tggccttcc cagcgcgggg gacgccaacg 780
38 acgagaagaa cgtgctgtcc ctgtggtttg acgggctcaa gctgctcgtc gtcaccgacg 840
39 gggacaaggg atgcaggtac ttaccaagg acttcaaggg cagcgtgccc ggcttcaagg 900
40 tcgacaccgt cgacaccacc ggcgcggggc acgccttcgt cggctccctc ctcgtcaacg 960
41 tcgccaagga cgactccatc ttccacaacg aggagaagct ccgcgaggct ctcaagttct 1020
42 ccaacgcctg cggcgccatc tgcaccacca agaagggcgc catcccggcg ctgcccacgg 1080
43 tcgcccacgc ccaggacctc atcgccaagg ccaactagat ggcgcgacgc cccgccgttc 1140
44 caccacgtca ctgtccccc cgcgcccgcc cctcgtcgtc gacgtcctcg gtttcggttc 1200
45 attaggtaga tcgagtctta gcgtccgtct ctgcgcctct acgtgagac ggtttgtttg 1260
46 ggttaattaa gttagctttc gtggagattt cgcgccgggg catcaataaa atgttggcat 1320
47 gcgtggtggg atgctatcct ttttttttat ttttttttat ttttttttta gcttggatca 1380
48 gttggggttt tgaacattgc tagtgctgtg tgattgggaa ggctaattgt atgccttoga 1440
49 tgcagagttt tcaatgaatg ccttggtgca aacgtaaaaa aaaaaaaaaa aaa 1493
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 371
54 <212> TYPE: PRT
55 <213> ORGANISM: Zea mays
57 <400> SEQUENCE: 2
58 Thr Arg Gln Ser Pro Arg Leu Pro Phe Pro Thr Ser Pro Ser Leu Ser
59 1 5 10 15

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61 Ser Leu Cys Leu Ser Ser Arg Asn Arg Val His Leu Ala Ala Ala Ser
62          20          25          30
64 Lys Arg Asp Gln Met Ala Pro Leu Gly Asp Gly Gly Ala Ala Ala Ala
65          35          40          45
67 Ala Ala Ser Asn Asn Leu Val Val Ser Phe Gly Glu Met Leu Ile Asp
68          50          55          60
70 Phe Val Pro Asp Val Ala Gly Leu Ser Leu Ala Glu Ser Gly Gly Phe
71 65          70          75          80
73 Val Lys Ala Pro Gly Gly Ala Pro Ala Asn Val Ala Cys Ala Ile Ala
74          85          90          95
76 Lys Leu Gly Gly Ser Ser Ala Phe Val Gly Lys Phe Gly Asp Asp Glu
77          100          105          110
79 Phe Gly His Met Leu Val Asn Ile Leu Lys Gln Asn Asn Val Asn Ser
80          115          120          125
82 Glu Gly Cys Leu Phe Asp Lys His Ala Arg Thr Ala Leu Ala Phe Val
83          130          135          140
85 Thr Leu Lys His Asp Gly Glu Arg Glu Phe Met Phe Tyr Arg Asn Pro
86 145          150          155          160
88 Ser Ala Asp Met Leu Thr Glu Ala Glu Leu Asp Leu Gly Leu Val
89          165          170          175
91 Arg Arg Ala Lys Val Phe His Tyr Gly Ser Ile Ser Leu Ile Ser Glu
92          180          185          190
94 Pro Cys Arg Ser Ala His Met Ala Ala Met Arg Ala Ala Lys Ala Ala
95          195          200          205
97 Gly Val Leu Cys Ser Tyr Asp Pro Asn Val Arg Leu Pro Leu Trp Pro
98          210          215          220
100 Ser Pro Asp Ala Ala Arg Glu Gly Ile Leu Ser Ile Trp Lys Glu Ala
101 225          230          235          240
103 Asp Phe Ile Lys Val Ser Asp Asp Glu Val Ala Phe Leu Thr Arg Gly
104          245          250          255
106 Asp Ala Asn Asp Glu Lys Asn Val Leu Ser Leu Trp Phe Asp Gly Leu
107          260          265          270
109 Lys Leu Leu Val Val Thr Asp Gly Asp Lys Gly Cys Arg Tyr Phe Thr
110          275          280          285
112 Lys Asp Phe Lys Gly Ser Val Pro Gly Phe Lys Val Asp Thr Val Asp
113          290          295          300
115 Thr Thr Gly Ala Gly Asp Ala Phe Val Gly Ser Leu Leu Val Asn Val
116 305          310          315          320
118 Ala Lys Asp Asp Ser Ile Phe His Asn Glu Lys Leu Arg Glu Ala
119          325          330          335
121 Leu Lys Phe Ser Asn Ala Cys Gly Ala Ile Cys Thr Thr Lys Lys Gly
122          340          345          350
124 Ala Ile Pro Ala Leu Pro Thr Val Ala Thr Ala Gln Asp Leu Ile Ala
125          355          360          365
127 Lys Ala Asn
128          370
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 430
133 <212> TYPE: DNA

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134 <213> ORGANISM: Zea mays
136 <220> FEATURE:
137 <221> NAME/KEY: unsure
138 <222> LOCATION: (293)
139 <223> OTHER INFORMATION: n = A, C, G or T
141 <400> SEQUENCE: 3
142 gcgacgacga gttcggccgc atgctcgccg ccatacctccg cgacaacggc gtcgacggcg 60
143 gcggcgctcgt cttcgacgcg ggcgcgcgca ccgccttgcc ttcgtcaccc tgcgcgcgca 120
144 cggcgagcgc gagttcatgt tctaccgcaa ccccgagcgc gacatgctcc tcaactgccga 180
145 cgagctcaac gtcgggctca tccggagggc tgcggtcttt cactacggat caataagctt 240
W--> 146 gattgctgag ccttgccgga cagcacatct ccgtgccatg gaaattgcc aanaaggctgg 300
147 tgcactgctc tcttacgacc caaacctgag ggaggcaatt tggccatccc gtgaggaggc 360
148 ccgcacccag atcttgagca ttgggaccag gcagatatcg tcaaggtcag cgaagtcgag 420
149 cttgagtttt 430
152 <210> SEQ ID NO: 4
153 <211> LENGTH: 101
154 <212> TYPE: PRT
155 <213> ORGANISM: Zea mays
157 <220> FEATURE:
158 <221> NAME/KEY: UNSURE
159 <222> LOCATION: (72)
160 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
162 <400> SEQUENCE: 4
163 Gly Arg Ala His Arg Leu Ala Phe Val Thr Leu Arg Ala Asp Gly Glu
164 1 5 10 15
166 Arg Glu Phe Met Phe Tyr Arg Asn Pro Ser Ala Asp Met Leu Leu Thr
167 20 25 30
169 Ala Asp Glu Leu Asn Val Gly Leu Ile Arg Arg Ala Ala Val Phe His
170 35 40 45
172 Tyr Gly Ser Ile Ser Leu Ile Ala Glu Pro Cys Arg Thr Ala His Leu
173 50 55 60
W--> 175 Arg Ala Met Glu Ile Ala Lys Xaa Ala Gly Ala Leu Leu Ser Tyr Asp
176 65 70 75 80
178 Pro Asn Leu Arg Glu Ala Leu Trp Pro Ser Arg Glu Glu Ala Arg Thr
179 85 90 95
181 Gln Ile Leu Ser Ile
182 100
185 <210> SEQ ID NO: 5
186 <211> LENGTH: 1553
187 <212> TYPE: DNA
188 <213> ORGANISM: Oryza sativa
190 <400> SEQUENCE: 5
191 gcacgagctt acactcatct catctcatct caccctcgcc gcgcgccgag gaagacgcgc 60
192 atctcctctc tccctctata taagcgcgcg cctcgccacc tcaccggaag aaattcccca 120
193 ccattccatc tctctctctc tcgaatcttg atctctctct ttcatcgctt cttgtgttcg 180
194 gcgcgcgcgag caggggtggtt gttgttggtg ggggtgcaat ggccggggagg agcgagctgg 240
195 tggtagcttt cggggagatg ctgatagact tctgcccgcg ggtggcgggg gtgtcgctgg 300
196 cggaggcgcc ggcgcttcgtc aaggcgccag ggggggcgcc ggccaacgtg gccatcgcg 360
197 tggcgcggtt cggcgggcggg gccgcgttcg tcggcaagct gggggacgac gaggttcggg 420

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198 ggatgctcgc ggccatcctc cgcgacaacg gcgtcgacga cggcgggggtc gtgttcgacg 480
199 cgggggcgcg caccgcgctc gccttcgtca cctccgcgc cgacggggag cgcgagttca 540
200 tgttctaccg caaccccagc gccgacatgc tctcaccga cgcgagctc aacgtcgagc 600
201 tcatcaagag ggctgccgtc ttccattatg gatcaataag cttagatagct gagccctgcc 660
202 ggtcagcaca ttgctgtgcc atggagattg cgaaagaagc tgggtgcgctg ctatcttatg 720
203 acccgaatct cagggaggca ttgtggccct cccgtgagga ggctcgacc aagatcttga 780
204 gcatctggga ccaggcagac attgtcaagg tcagcgaggt cgagcttgag ttcttgaccg 840
205 gcattgactc agtagaggat gatgttgtca tgaagctatg gcgccctacc atgaagctcc 900
206 tccttgtgac tcttgagat caaggatgca agtactatgc cagggatttc cgcggagctg 960
207 tcccatccta caaagtacag caagttgata caacaggtgc aggtgatgcg tttgttggtg 1020
208 ctctgctgcg aagaattgtc caggatccat catcgttgca agatcagaag aagcttgagg 1080
209 aagcgattaa atttgccaat gcgtgaggag caatcaccgc cacaagaaa ggggcaatcc 1140
210 catcactgcc caccgaagtt gaggtcttga agttgatgga gagtgcctag atcgatcagt 1200
211 agcattatgg tctactagctt cagcttccgc aaattgtatt gtatgctgat ctggatcagg 1260
212 agcagggggg tactccaaga tgctgcctt tttgttgcca acttcccttc ctggcaggat 1320
213 ttttgatttg gaactcta at ttgaataagc agagccgttc aatgtcagtt tctactatat 1380
214 gattaaataa tcggctocta attgtaatgc atcattcttt tttttttttt aactgaatcc 1440
215 ttgttccatg ctgtatgaac tcctttgagt tccatttgta tatggtgctc ttgccattat 1500
216 aagagtagtg tttggtccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1553

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219 <210> SEQ ID NO: 6

220 <211> LENGTH: 368

221 <212> TYPE: PRT

222 <213> ORGANISM: Oryza sativa

224 <400> SEQUENCE: 6

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226   1           5           10           15
228 Leu Ser Leu Ser Asn Leu Asp Leu Ser Leu Ser Ser Pro Leu Val Phe
229           20           25           30
231 Ala Arg Ala Ser Arg Val Val Val Val Gly Gly Gly Ala Met Ala Gly
232           35           40           45
234 Arg Ser Glu Leu Val Val Ser Phe Gly Glu Met Leu Ile Asp Phe Val
235           50           55           60
237 Pro Thr Val Ala Gly Val Ser Leu Ala Glu Ala Pro Ala Phe Val Lys
238           65           70           75           80
240 Ala Pro Gly Gly Ala Pro Ala Asn Val Ala Ile Ala Val Ala Arg Leu
241           85           90           95
243 Gly Gly Gly Ala Ala Phe Val Gly Lys Leu Gly Asp Asp Glu Phe Gly
244           100          105          110
246 Arg Met Leu Ala Ala Ile Leu Arg Asp Asn Gly Val Asp Asp Gly Gly
247           115          120          125
249 Val Val Phe Asp Ala Gly Ala Arg Thr Ala Leu Ala Phe Val Thr Leu
250           130          135          140
252 Arg Ala Asp Gly Glu Arg Glu Phe Met Phe Tyr Arg Asn Pro Ser Ala
253           145          150          155          160
255 Asp Met Leu Leu Thr His Ala Glu Leu Asn Val Glu Leu Ile Lys Arg
256           165          170          175
258 Ala Ala Val Phe His Tyr Gly Ser Ile Ser Leu Ile Ala Glu Pro Cys
259           180          185          190
261 Arg Ser Ala His Leu Arg Ala Met Glu Ile Ala Lys Glu Ala Gly Ala

```

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Input Set : A:\BB1470 US NA Seq listing.txt

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```

262          195          200          205
264 Leu Leu Ser Tyr Asp Pro Asn Leu Arg Glu Ala Leu Trp Pro Ser Arg
265          210          215          220
267 Glu Glu Ala Arg Thr Lys Ile Leu Ser Ile Trp Asp Gln Ala Asp Ile
268 225          230          235          240
270 Val Lys Val Ser Glu Val Glu Leu Glu Phe Leu Thr Gly Ile Asp Ser
271          245          250          255
273 Val Glu Asp Asp Val Val Met Lys Leu Trp Arg Pro Thr Met Lys Leu
274          260          265          270
276 Leu Leu Val Thr Leu Gly Asp Gln Gly Cys Lys Tyr Tyr Ala Arg Asp
277          275          280          285
279 Phe Arg Gly Ala Val Pro Ser Tyr Lys Val Gln Gln Val Asp Thr Thr
280          290          295          300
282 Gly Ala Gly Asp Ala Phe Val Gly Ala Leu Leu Arg Arg Ile Val Gln
283 305          310          315          320
285 Asp Pro Ser Ser Leu Gln Asp Gln Lys Lys Leu Glu Glu Ala Ile Lys
286          325          330          335
288 Phe Ala Asn Ala Cys Gly Ala Ile Thr Ala Thr Lys Lys Gly Ala Ile
289          340          345          350
291 Pro Ser Leu Pro Thr Glu Val Glu Val Leu Lys Leu Met Glu Ser Ala
292          355          360          365
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 1310
297 <212> TYPE: DNA
298 <213> ORGANISM: Glycine max
300 <400> SEQUENCE: 7
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302 ctctctcccc atggcggttg acaatggcgt ccccgccacc ggcaaccggc tcatcgctcag 120
303 cttcggtgag atgctcatcg acttcgtccc caccgtctct ggcggtgtcc tggccgaggc 180
304 ccctggcttc ctcaaggccc ccggcggcgc ccccgctaac gtcgccatcg ccgtgtcgcg 240
305 cctcggcggc aaagccgcct tcgtcggcaa gctcggcgac gacgagttcg gccacatgct 300
306 cgccggaatc ctcaaggaaa acggcggttc cgccgacggc atcaactttg accagggcgc 360
307 acgcaccgcc ctggccttcg tgaccctacg cgccgacggg gagcgtgagt tcatgttcta 420
308 cagaaacccc agcgcgcaca tgctcctcaa gccgaagaa ctcaatctcg aactcatcag 480
309 atctgcaaaa gttttccatt acggatcaat cagtttgatc gtggagccat gcagatcagc 540
310 acacttgaag gcaatggaag tagccaagga atctgggtgc ttgctctcct atgaccccaa 600
311 ccttcgtcta cctttgtggc cttcggctga ggaagctcgt aagcaaatac tgagcatttg 660
312 ggagaaggct gatttgatca aggtcagtga tgcggagctt gagttcctca caggaagtga 720
313 caagattgat gatgaatctg ctttgtcatt gtggcacccc aatttgaagt tgctccttgt 780
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315 tttccatgtc aatacagttg atacaactgg tgccggtgat tcctttgttg gtgctttatt 900
316 ggccaagatt gtcgatgatc agtccatact tgaagatgaa ccaaggttaa gagaagtact 960
317 aaagtttgca aatgcatgtg gagctattac aactacccaa aaggagcaa ttccggccct 1020
318 tcccaaagag gaggctgcac tgaaactgat caaagggggg tcatagaatc tttggcaaa 1080
319 atgcaaaagt gctagcatga tttcgttttc ttcccctaata gtttaaattt tccgttggat 1140
320 ttgcttgcta taagtttagg agggaaacttt tgttttttct cctatgcact gttttcaggt 1200
321 tttgccaaat aacgctttct ttcaaatttt gagattagcg attgaatgaa aatttgaatc 1260
322 ataagctcgg cccatagttg caacttaaaa aaaaaaaaaa aaaaaaaaaa 1310
325 <210> SEQ ID NO: 8

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VERIFICATION SUMMARY

DATE: 12/12/2001

PATENT APPLICATION: US/10/004,502

TIME: 14:28:18

Input Set : A:\BB1470 US NA Seq listing.txt

Output Set: N:\CRF3\12112001\I004502.raw

L:5 M:201 W: Mandatory field data missing, TITLE INVENTION
L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4